SEQUENCE LISTING

(1) GENERAL INFORMATION:

5   (i)   APPLICANT: ANDREW C. HIATT, JULIAN
                                         K.-C. MA, THOMAS LEHNER

         (ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
                                         PROTEINS IN PLANTS AND THEIR USES
10

         (iii) NUMBER OF SEQUENCES: 19

         (iv) CORRESPONDENCE ADDRESS:

15   (A) ADDRESSEE: Lyon & Lyon
               (B) STREET: 633 West Fifth Street
                                         Suite 4700
               (C) CITY: Los Angeles
               (D) STATE: California
20   (E) COUNTRY: U.S.A.
               (F) ZIP: 90071

         (v)   COMPUTER READABLE FORM:

25   (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                         storage
               (B) COMPUTER: IBM Compatible
               (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
               (D) SOFTWARE: Word Perfect 5.1
30
         (vi) CURRENT APPLICATION DATA:

               (A) APPLICATION NUMBER: TO BE ASSIGNED
               (B) FILING DATE:
35   (C) CLASSIFICATION:

         (vii) PRIOR APPLICATION DATA:

               Prior applications total,
40   including application
               described below: 1

         U.S. Patent Application Serial No. 08/367,395
         Filed 12/30/94
45   Docket No. 210/152

(viii) ATTORNEY/AGENT INFORMATION:

      (A) NAME: Guise, Jeffrey W.
      (B) REGISTRATION NUMBER: 34,613
      (C) REFERENCE/DOCKET NUMBER: 212/127

(ix) TELECOMMUNICATION INFORMATION:

      (A) TELEPHONE: (619) 552-8400
      (B) TELEFAX: (619) 552-0159
      (C) TELEX: 67-3510

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 3517 base pairs
10   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
             DESCRIPTION: Rabbit polyimmunoglobulin receptor

15   (ix) FEATURE:

        (A) NAME/KEY: Coding Sequence
        (B) LOCATION: 124....2445

20   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

    GGCCGGGGTT ACGGGCTGGC CAGCAGGCTG TGCCCCCGAG TCCGGTCAGCAGGAGGGGAA   60

    GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA   120
25
    GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG   168
        Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala
        1   5   10   15

30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC   216
    Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro
                    20   25   30

    GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC   264
35 Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
                        35   40   45

    TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG   312
    Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg
40   50   55   60

    GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG   360
    Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr
        65   70   75
45
    TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA   408
    Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys
    80   85   90   95

50 GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG   456
    Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly
                        100   105   110

    AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT   504
55 Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly
                    115   120   125

    GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC   552
    Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr
60   130   135   140

    AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT   600
    Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr
                145   150   155
65
    GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA   648

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       Ala Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu
       160             165             170             175

   5   CTT GTA CTC ATC ATT GAT TCC AGC AGT AAG GAG GCA AAG GAC CCC AGG    696
       Leu Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg
                           180             185             190

       TAT AAG GGC AGA ATA ACG TTG CAG ATC CAA AGT ACC ACA GCA AAA GAA    744
  10   Tyr Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu
                   195             200             205

       TTC ACA GTC ACC ATC AAG CAT TTG CAG CTC AAT GAT GCT GGG CAG TAT    792
       Phe Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr
  15               210             215             220

       GTC TGC CAG AGT GGA AGC GAC CCC ACT GCT GAA GAA CAG AAC GTT GAC    840
       Val Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp
                   225             230             235

  20   CTC CGA CTG CTA ACT CCT GGT CTG CTC TAT GGA AAC CTG GGG GGC TCG    888
       Leu Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser
       240             245             250             255

       GTG ACC TTT GAA TGT GCC CTG GAC TCT GAA GAC GCA AAC GCG GTA GCA    936
  25   Val Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala
                       260             265             270

       TCC TTG CGC CAG GTT AGG GGT GGC AAT GTG GTC ATT GAC AGC CAG GGG    984
       Ser Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly
  30                   275             280             285

       ACA ATA GAT CCA GCC TTC GAG GGC AGG ATC CTG TTC ACC AAG GCT GAG   1032
       Thr Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu
                   290             295             300
  35
       AAC GGC CAC TTC AGT GTA GTG ATC GCA GGC CTG AGG AAG GAA GAC ACA   1080
       Asn Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr
                   305             310             315

  40   GGG AAC TAT CTG TGC GGA GTC CAG TCC AAT GGT CAG TCT GGG GAT GGG   1128
       Gly Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly
       320             325             330             335

       CCC ACC CAG CTT CGG CAA CTC TTC GTC AAT GAA GAG ATC GAC GTG TCC   1176
  45   Pro Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser
                       340             345             350

       CGC AGC CCC CCT GTG TTG AAG GGC TTT CCA GGA GGC TCC GTG ACC ATA   1224
       Arg Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile
  50               355             360             365

       CGC TGC CCC TAC AAC CCG AAG AGA AGC GAC AGC CAC CTG CAG CTG TAT   1272
       Arg Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr
                   370             375             380
  55
       CTC TGG GAA GGG AGT CAA ACC CGC CAT CTG CTG GTG GAC AGC GGC GAG   1320
       Leu Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu
                   385             390             395

  60   GGG CTG GTT CAG AAA GAC TAC ACA GGC AGG CTG GCC CTG TTC GAA GAG   1368
       Gly Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu
       400             405             410             415

       CCT GGC AAT GGC ACC TTC TCA GTC GTC CTC AAC CAG CTC ACT GCC GAG   1416
  65   Pro Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu
                       420             425             430
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   GAT GAA GGC TTC TAC TGG TGT GTC AGC GAT GAC GAT GAG TCC CTG ACG    1464
   Asp Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr
               435             440             445

5  ACT TCG GTG AAG CTC CAG ATC GTT GAC GGA GAA CCA AGC CCC ACG ATC    1512
   Thr Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile
               450             455             460

   GAC AAG TTC ACT GCT GTG CAG GGA GAG CCT GTT GAG ATC ACC TGC CAC    1560
10 Asp Lys Phe Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys His
               465             470             475

   TTC CCA TGC AAA TAC TTC TCC TCC GAG AAG TAC TGG TGC AAG TGG AAT    1608
   Phe Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn
15 480             485             490             495

   GAC CAT GGC TGC GAG GAC CTG CCC ACT AAG CTC AGC TCC AGC GGC GAC    1656
   Asp His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp
               500             505             510
20
   CTT GTG AAA TGC AAC AAC AAC CTG GTC CTC ACC CTG ACC TTG GAC TCG    1704
   Leu Val Lys Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser
               515             520             525

25 GTC AGC GAA GAT GAC GAG GGC TGG TAC TGG TGT GGC GCG AAA GAC GGG    1752
   Val Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly
               530             535             540

   CAC GAG TTT GAA GAG GTT GCG GCC GTC AGG GTG GAG CTG ACA GAG CCA    1800
30 His Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro
               545             550             555

   GCC AAG GTA GCT GTC GAG CCA GCC AAG GTA CCT GTC GAC CCA GCC AAG    1848
   Ala Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys
35 560             565             570             575

   GCA GCC CCC GCG CCT GCT GAG GAG AAG GCC AAG GCG CGG TGC CCA GTG    1896
   Ala Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val
               580             585             590
40
   CCC AGG AGA AGG CAG TGG TAC CCA TTG TCA AGG AAG CTG AGA ACA AGT    1944
   Pro Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser
               595             600             605

45 TGT CCA GAA CCT CGG CTC CTT GCG GAG GAG GTA GCA GTG CAG AGT GCG    1992
   Cys Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala
               610             615             620

   GAA GAC CCA GCC AGT GGG AGC AGA GCG TCT GTG GAT GCC AGC AGT GCT    2040
50 Glu Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala
               625             630             635

   TCG GGA CAA AGC GGG AGT GCC AAA GTA CTG ATC TCC ACC CTG GTG CCC    2088
   Ser Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro
55 640             645             650             655

   TTG GGG CTG GTG CTG GCA GCG GGG GCC ATG GCC GTG GCC ATA GCC AGA    2136
   Leu Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg
               660             665             670
60
   GCC CGG CAC AGG AGG AAC GTG GAC CGA GTT TCC ATC GGA AGC TAC AGG    2184
   Ala Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg
               675             680             685

65 ACA GAC ATT AGC ATG TCA GAC TTG GAG AAC TCC AGG GAG TTC GGA GCC    2232
   Thr Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala
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                690                    695                    700

        ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GGC CTC GGA    2280
        Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly
   5        705                 710                 715

        GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG    2328
        Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu
        720  .             725                 730                 735
  10

        GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC    2376
        Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala
                        740                 745                 750

  15    TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA    2424
        Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln
                        755                 760                 765

        GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC    2480
  20    Asp Gly Pro Lys Glu Ala
                        770

        CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAATCACGT TGATCCTCGG GGTCCCCAGA    2540

  25    GCCGGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT    2600

        GCCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCATCCAGG CCTGGCTCAA TGTTCCCGTT    2660

        GGGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCCGGTTC TCCCGAGAGA AGCTAAGGAT    2720
  30
        CCAGGTCCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT    2780

        TGGATGGGAG GCCAGAGGCG CTTTCCGGCC ACCCCCTCCC TCCCTGCCCC CACCCTCCTT    2840

  35    CCTTCATTCA AAAGTCCCAG TGGCTGCTGC CTAGGGTCCA GGCGCTGGCC GCACGCCTCC    2900

        TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC    2960

        TCACTCAGGC ATCCTGTCCT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG    3020
  40
        CCCTGGGCGT GTCTGCAAGT CACCCCAGAC ACATGTTCTC GCCATTTTAC AGATGAGAAC    3080

        ACTGAGGTTG TACTCAAGGG CACCCTGCGA GATGGAGCAA CAGCAAACTA GATGGGCTTC    3140

  45    TGCTGTCCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCCT GCCCCTGTAG GAAGCAGAGT    3200

        TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC    3260

        ACGGGGGAAA AGGCCCCCTC CTTTTCTGTC ACTCTCGGGG ACCTGCGGAG TTGAGCATTC    3320
  50
        GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC    3380

        CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGGTC CTTGTCCCTG TGAGCTTTAA    3440

  55    CCAGCACCTC CGGGCTGACC CTTGCTAACA CATCAGAAAT GTGATTTAAT CATTAAACAT    3500

        TGTGATTGCC ACTGGGA                                                   3517
```

  60

  (2) INFORMATION FOR SEQ ID NO: 2:

          (i) SEQUENCE CHARACTERISTICS:

  65   (A) LENGTH: 773 amino acids

```
(B)    TYPE:           amino acid
(C)    STRANDNESS:     single
(D)    TOPOLOGY:       linear
       DESCRIPTION:    Rabbit polyimmunoglobulin receptor
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala Ala
1               5                  10                  15

Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly
            20                  25                  30

Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr
        35                  40                  45

Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu
    50                  55                  60

Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser
65                  70                  75                  80

Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly
                85                  90                  95

Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser
                100                 105                 110

Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly Val
        115                 120                 125

Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr Lys
    130                 135                 140

Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala
145                 150                 155                 160

Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu
            165                 170                 175

Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr
                180                 185                 190

Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe
        195                 200                 205

Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val
    210                 215                 220

Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp Leu
225                 230                 235                 240

Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser Val
            245                 250                 255

Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala Ser
            260                 265                 270

Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly Thr
        275                 280                 285

Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu Asn
    290                 295                 300

Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr Gly
305                 310                 315                 320
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```
     Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly Pro
                     325             330             335

  5  Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser Arg
                 340             345             350

     Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile Arg
             355             360             365

 10  Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr Leu
         370             375             380

     Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu Gly
     385             390             395             400

 15  Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu Pro
                 405             410             415

 20  Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu Asp
                 420             425             430

     Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr Thr
             435             440             445

 25  Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile Asp
         450             455             460

     Lys Phe Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys His Phe
     465             470             475             480

 30  Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn Asp
                 485             490             495

 35  His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp Leu
             500             505             510

     Val Lys Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser Val
         515             520             525

 40  Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly His
         530             535             540

     Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro Ala
     545             550             555             560

 45  Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys Ala
                 565             570             575

 50  Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val Pro
                 580             585             590

     Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser Cys
             595             600             605

 55  Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala Glu
         610             615             620

     Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala Ser
     625             630             635             640

 60  Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro Leu
                 645             650             655

 65  Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg Ala
                 660             665             670
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    Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg Thr
            675             680             685

 5  Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala Ile
            690             695             700

    Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly Gly
    705             710             715             720

10  Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu Glu
                    725             730             735

    Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala Tyr
                740             745             750

15  Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln Asp
                755             760             765

20  Gly Pro Lys Glu Ala
            770
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    AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG    60

    GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG   120
45
    GCTAAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA   180

    ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACG AAG     237
                                                              Lys
50                                                             1

    AGT CCC ATA TTT GGT CCC GAG GAG GTG AAT AGT GTG GAA GGT AAC TCA    285
    Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn Ser
                5               10              15
55
    GTG TCC ATC ACG TGC TAC TAC CCA CCC ACC TCT GTC AAC CGG CAC ACC    333
    Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr
            20              25              30

60  CGG AAG TAC TGG TGC CGG CAG GGA GCT AGA GGT GGC TGC ATA ACC CTC    381
    Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr Leu
            35              40              45

    ATC TCC TCG GAG GGC TAC GTC TCC AGC AAA TAT GCA GGC AGG GCT AAC    429
65  Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala Asn
    50              55              60              65
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    CTC ACC AAC TTC CCG GAG AAC GGC ACA TTT GTG GTG AAC ATT GCC CAG        477
    Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala Gln
                     70                  75                  80

5   CTG AGC CAG GAT GAC TCC GGG CGC TAC AAG TGT GGC CTG GGC ATC AAT        525
    Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Asn
                     85                  90                  95

10  AGC CGA GGC CTG TCC TTT GAT GTC AGC CTG GAG GTC AGC CAG GGT CCT        573
    Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly Pro
                    100                 105                 110

    GGG CTC CTA AAT GAC ACT AAA GTC TAC ACA GTG GAC CTG GGC AGA ACG        621
    Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg Thr
15          115                 120                 125

    GTG ACC ATC AAC TGC CCT TTC AAG ACT GAG AAT GCT CAA AAG AGG AAG        669
    Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg Lys
    130                 135                 140                 145
20

    TCC TTG TAC AAG CAG ATA GGC CTG TAC CCT GTG CTG GTC ATC GAC TCC        717
    Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp Ser
                    150                 155                 160

25  AGT GGT TAT GTG AAT CCC AAC TAT ACA GGA AGA ATA CGC CTT GAT ATT        765
    Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp Ile
                    165                 170                 175

    CAG GGT ACT GGC CAG TTA CTG TTC AGC GTT GTC ATC AAC CAA CTC AGG        813
30  Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu Arg
                    180                 185                 190

    CTC AGC GAT GCT GGG CAG TAT CTC TGC CAG GCT GGG GAT GAT TCC AAT        861
    Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser Asn
35          195                 200                 205

    AGT AAT AAG AAG AAT GCT GAC CTC CAA GTG CTA AAG CCC GAG CCC GAG        909
    Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro Glu
    210                 215                 220                 225
40

    CTG GTT TAT GAA GAC CTG AGG GGC TCA GTG ACC TTC CAC TGT GCC CTG        957
    Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala Leu
                    230                 235                 240

45  GGC CCT GAG GTG GCA AAC GTG GCC AAA TTT CTG TGC CGA CAG AGC AGT       1005
    Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser Ser
                    245                 250                 255

    GGG GAA AAC TGT GAC GTG GTC GTC AAC ACC CTG GGG AAG AGG GCC CCA       1053
50  Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala Pro
                    260                 265                 270

    GCC TTT GAG GGC AGG ATC CTG CTC AAC CCC CAG GAC AAG GAT GGC TCA       1101
    Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly Ser
55          275                 280                 285

    TTC AGT GTG GTG ATC ACA GGC CTG AGG AAG GAG GAT GCA GGG CGC TAC       1149
    Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg Tyr
    290                 295                 300                 305
60

    CTG TGT GGA GCC CAT TCG GAT GGT CAG CTG CAG GAA GGC TCG CCT ATC       1197
    Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro Ile
                    310                 315                 320

65  CAG GCC TGG CAA CTC TTC GTC AAT GAG GAG TCC ACG ATT CCC CGC AGC       1245
    Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg Ser
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                  325                    330                    335
         CCC ACT GTG GTG AAG GGG GTG GCA GGA AGC TCT GTG GCC GTG CTC TGC    1293
     5   Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu Cys
                 340                 345                 350

         CCC TAC AAC CGT AAG GAA AGC AAA AGC ATC AAG TAC TGG TGT CTC TGG    1341
         Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu Trp
    10           355                 360                 365

         GAA GGG GCC CAG AAT GGC CGC TGC CCC CTG CTG GTG GAC AGC GAG GGG    1389
         Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu Gly
         370                 375                 380                 385

    15   TGG GTT AAG GCC CAG TAC GAG GGC CGC CTC TCC CTG CTG GAG GAG CCA    1437
         Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu Pro
                         390                 395                 400

         GGC AAC GGC ACC TTC ACT GTC ATC CTC AAC CAG CTC ACC AGC CGG GAC    1485
    20   Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg Asp
                     405                 410                 415

         GCC GGC TTC TAC TGG TGT CTG ACC AAC GGC GAT ACT CTC TGG AGG ACC    1533
         Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg Thr
    25               420                 425                 430

         ACC GTG GAG ATC AAG ATT ATC GAA GGA GAA CCA AAC CTC AAG GTA CCA    1581
         Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val Pro
                 435                 440                 445
    30
         GGG AAT GTC ACG GCT GTG CTG GGA GAG ACT CTC AAG GTC CCC TGT CAC    1629
         Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys His
         450                 455                 460                 465

    35   TTT CCA TGC AAA TTC TCC TCG TAC GAG AAA TAC TGG TGC AAG TGG AAT    1677
         Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp Asn
                         470                 475                 480

         AAC ACG GGC TGC CAG GCC CTG CCC AGC CAA GAC GAA GGC CCC AGC AAG    1725
    40   Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser Lys
                     485                 490                 495

         GCC TTC GTG AAC TGT GAC GAG AAC AGC CGG CTT GTC TCC CTG ACC CTG    1773
         Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr Leu
    45           500                 505                 510

         AAC CTG GTG ACC AGG GCT GAT GAG GGC TGG TAC TGG TGT GGA GTG AAG    1821
         Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys
                 515                 520                 525
    50
         CAG GGC CAC TTC TAT GGA GAG ACT GCA GCC GTC TAT GTG GCA GTT GAA    1869
         Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu
         530                 535                 540                 545

    55   GAG AGG AAG GCA GCG GGG TCC CGC GAT GTC AGC CTA GCG AAG GCA GAC    1917
         Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala Asp
                         550                 555                 560

         GCT GCT CCT GAT GAG AAG GTG CTA GAC TCT GGT TTT CGG GAG ATT GAG    1965
    60   Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile Glu
                     565                 570                 575

         AAC AAA GCC ATT CAG GAT CCC AGG CTT TTT GCA GAG GAA AAG GCG GTG    2013
         Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val
    65           580                 585                 590
```

```
GCA GAT ACA AGA GAT CAA GCC GAT GGG AGC AGA GCA TCT GTG GAT TCC    2061
Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp Ser
    595                     600                 605

GGC AGC TCT GAG GAA CAA GGT GGA AGC TCC AGA GCG CTG GTC TCC ACC    2109
Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg Ala Leu Val Ser Thr
610                     615                 620                 625

CTG GTG CCC CTG GGC CTG GTG CTG GCA GTG GGA GCC GTG GCT GTG GGG    2157
Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Gly
                630                 635                 640

GTG GCC AGA GCC CGG CAC AGG AAG AAC GTC GAC CGA GTT TCA ATC AGA    2205
Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile Arg
            645                 650                 655

AGC TAC AGG ACA GAC ATT AGC ATG TCA GAC TTC GAG AAC TCC AGG GAA    2253
Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Glu
        660                 665                 670

TTT GGA GCC AAT GAC AAC ATG GGA GCC TCT TCG ATC ACT CAG GAG ACA    2301
Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr
    675                 680                 685

TCC CTC GGA GGA AAA GAA GAG TTT GTT GCC ACC ACT GAG AGC ACC ACA    2349
Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr
690                 695                 700                 705

GAG ACC AAA GAA CCC AAG AAG GCA AAA AGG TCA TCC AAG GAG GAA GCC    2397
Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala
            710                 715                 720

GAG ATG GCC TAC AAA GAC TTC CTG CTC CAG TCC AGC ACC GTG GCC GCC    2445
Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala
            725                 730                 735

GAG GCC CAG GAC GGC CCC CAG GAA GCC TAGACGGTGT CGCCGCCTGC TCCCTGCA  2500
Glu Ala Gln Asp Gly Pro Gln Glu Ala
            740                 745

CCCATGACAA TCACCTTCAG AATCATGTCG ATCCTGGGGG CCCTCAGCTC CTGGGGACCC    2560

CACTCCCTGC TCTAACACCT GCCTAGGTTT TTCCTACTGT CCTCAGAGGC GTGCTGGTCC    2620

CCTCCTCAGT GACATCAAAG CCTGGCCTAA TTGTTCCTAT TGGGGATGAG GGTGGCATGA    2680

GGAGGTCCCA CTTGCAACTT CTTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG    2740

GTCCTCATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA    2800

GAGACGTGCA GCGCCCCTCT GCACCCTTAT CATGGGATGT CAACAGAATT TTTTCCCTCC    2860

ACTCCATCCC TCCCTCCCGT CCTTCCCCTC TTCTTCTTTC CTTACCATCA AAAGATGTA     2919
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 746 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDNESS: single
        (D)   TOPOLOGY: linear
            DESCRIPTION: Human Polyimmunoglbulin Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```
Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn
 1           5               10              15
Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His
             20              25              30
Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr
         35              40              45
Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala
         50              55              60
Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala
 65              70              75              80
Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile
             85              90              95
Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly
         100             105             110
Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg
         115             120             125
Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg
     130             135             140
Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp
     145             150             155             160
Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp
             165             170             175
Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu
             180             185             190
Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser
         195             200             205
Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro
     210             215             220
Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala
     225             230             235             240
Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser
             245             250             255
Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala
             260             265             270
Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly
         275             280             285
Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg
         290             295             300
Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro
     305             310             315             320
Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg
             325             330             335
Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu
```

```
                    340                 345                 350

        Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu
                355                 360                 365
    5

        Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu
            370                 375                 380

        Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu
   10   385                 390                 395                 400

        Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg
                        405                 410                 415

   15   Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg
                        420                 425                 430

        Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val
                    435                 440                 445
   20
        Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys
                450                 455                 460

        His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp
   25   465                 470                 475                 480

        Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser
                        485                 490                 495

   30   Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr
                        500                 505                 510

        Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val
                515                 520                 525
   35
        Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val
                530                 535                 540

        Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala
   40   545                 550                 555                 560

        Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile
                        565                 570                 575

   45   Glu Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala
                        580                 585                 590

        Val Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp
                        595                 600                 605
   50
        Ser Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg Ala Leu Val Ser
                610                 615                 620

        Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val
   55   625                 630                 635                 640

        Gly Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile
                        645                 650                 655

   60   Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg
                        660                 665                 670

        Glu Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu
                675                 680                 685
   65
        Thr Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr
```

```
        690                    695                   700

      Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu
      705                 710                 715                 720
  5

      Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala
                      725             730                 735

      Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala
 10                   740                 745
```

(2) INFORMATION FOR SEQ ID NO: 5:

 15
           (i)   SEQUENCE CHARACTERISTICS:

                 (A)   LENGTH: 3630 base pairs
                 (B)   TYPE: nucleic acid
 20   (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY: linear
                       DESCRIPTION: Bovine Polyimmunoglobulin Receptor

           (ix) FEATURE:
 25
                 (A)   NAME/KEY: Coding Sequence
                 (B)   LOCATION: 152....2425

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 30
```
GATCTCCTCG GAGGGTCGTG CAGCGGCCCT GGGTCCCTGC CGGCACCAGT ACTTGCGCGT    60

GTGCTCCCAA AGCTGACGGG ATAGGAGGAA GGAGCTCAAA CAACCACACA GGACGGTGGC   120
```
 35
```
TGGCGGCAGA GACCCGCGGG AGCCCCCAGC G ATG TCG CGC CTG TTC CTC GCC       172
                                   Met Ser Arg Leu Phe Leu Ala
                                    1               5
```

```
      TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC   220
 40   Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe
                  10              15                  20
```

```
      GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG   268
      Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys
 45    25                  30                  35
```

```
      TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG   316
      Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp
       40                  45                  50                  55
 50
      TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG   364
      Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu
                      60                  65                  70
```

```
 55   GGC TAC GTC TCC GAC GAC TAC GTG GGC AGA GCC AAC CTC ACC AAC TTC   412
      Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe
                      75                  80                  85
```

```
      CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA   460
 60   Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys
                  90                  95                  100
```

```
      GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT   508
      Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu
 65    105                 110                 115
```

```
     AAC TTC GAT GTG AGC CTG GAG GTC AGC CAA GAT CCT GCA CAG GCA AGT        556
     Asn Phe Asp Val Ser Leu Glu Val Ser Gln Asp Pro Ala Gln Ala Ser
     120             125                 130                 135

  5  CAT GCC CAC GTC TAC ACT ATA GAC CTG GGC AGG ACT GTG ACC ATC AAC        604
     His Ala His Val Tyr Thr Ile Asp Leu Gly Arg Thr Val Thr Ile Asn
                     140                 145                 150

     TGC CCT TTC ACG CGT GCG AAT TCT GAG AAG AGA AAA TCC TTG TGC AAG        652
 10  Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys
                     155                 160                 165

     AAG ACA ATC CAG GAC TGT TTC CAA GTT GTC GAC TCC ACC GGG TAT GTG        700
     Lys Thr Ile Gln Asp Cys Phe Gln Val Val Asp Ser Thr Gly Tyr Val
 15              170                 175                 180

     AGC AAC AGC TAT AAA GAC AGA GCA CAT ATC AGT ATC CTA GGT ACC AAC        748
     Ser Asn Ser Tyr Lys Asp Arg Ala His Ile Ser Ile Leu Gly Thr Asn
                 185                 190                 195
 20
     ACA TTA GTG TTC AGC GTT GTC ATC AAC CGA GTC AAG CTC AGT GAT GCT        796
     Thr Leu Val Phe Ser Val Val Ile Asn Arg Val Lys Leu Ser Asp Ala
     200             205                 210                 215

 25  GGG ATG TAT GTC TGC CAG GCT GGG GAC GAT GCC AAA GCC GAT AAA ATC        844
     Gly Met Tyr Val Cys Gln Ala Gly Asp Asp Ala Lys Ala Asp Lys Ile
                     220                 225                 230

     AAC ATT GAC CTC CAG GTG CTG GAG CCT GAG CCT GAG CTG GTT TAT GGA        892
 30  Asn Ile Asp Leu Gln Val Leu Glu Pro Glu Pro Glu Leu Val Tyr Gly
                     235                 240                 245

     GAC TTG AGG AGC TCG GTG ACC TTT GAC TGT TCC CTG GGC CCC GAG GTG        940
     Asp Leu Arg Ser Ser Val Thr Phe Asp Cys Ser Leu Gly Pro Glu Val
 35              250                 255                 260

     GCA AAT GTG CCC AAA TTT CTG TGC CAG AAG AAG AAT GGG GGA GCT TGC        988
     Ala Asn Val Pro Lys Phe Leu Cys Gln Lys Lys Asn Gly Gly Ala Cys
                 265                 270                 275
 40
     AAT GTA GTC ATC AAC ACG TTG GGG AAG AAG GCT CAG GAC TTC CAG GGC       1036
     Asn Val Val Ile Asn Thr Leu Gly Lys Lys Ala Gln Asp Phe Gln Gly
     280             285                 290                 295

 45  AGG ATC GTG TCC GTG CCC AAG GAC AAT GGT GTC TTC AGT GTG CAC ATT       1084
     Arg Ile Val Ser Val Pro Lys Asp Asn Gly Val Phe Ser Val His Ile
                     300                 305                 310

     ACC AGC CTG AGG AAA GAG GAC GCA GGG CGC TAC GTG TGC GGG GCC CAG       1132
 50  Thr Ser Leu Arg Lys Glu Asp Ala Gly Arg Tyr Val Cys Gly Ala Gln
                     315                 320                 325

     CCT GAG GGT GAG CCC CAG GAC GGC TGG CCT GTG CAG GCC TGG CAA CTC       1180
     Pro Glu Gly Glu Pro Gln Asp Gly Trp Pro Val Gln Ala Trp Gln Leu
 55              330                 335                 340

     TTC GTC AAT GAA GAG ACG GCA ATC CCC GCA AGC CCC TCC GTG GTG AAA       1228
     Phe Val Asn Glu Glu Thr Ala Ile Pro Ala Ser Pro Ser Val Val Lys
                 345                 350                 355
 60
     GGT GTG AGG GGA GGC TCT GTG ACT GTA TCT TGC CCC TAC AAC CCT AAG       1276
     Gly Val Arg Gly Gly Ser Val Thr Val Ser Cys Pro Tyr Asn Pro Lys
     360             365                 370                 375

 65  GAT GCC AAC AGC GCG AAG TAC TGG TGT CAC TGG GAA GAG GCT CAA AAC       1324
     Asp Ala Asn Ser Ala Lys Tyr Trp Cys His Trp Glu Glu Ala Gln Asn
```

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                    380                    385                    390
     GGC CGC TGC CCG CGG CTG GTG GAG AGC CGG GGG CTG ATG AAG GAG CAG    1372
     Gly Arg Cys Pro Arg Leu Val Glu Ser Arg Gly Leu Met Lys Glu Gln
 5                   395                400                405

     TAC GAG GGC AGG CTG GTG CTG CTC ACC GAG CCG GGC AAC GGC ACC TAC    1420
     Tyr Glu Gly Arg Leu Val Leu Leu Thr Glu Pro Gly Asn Gly Thr Tyr
                 410                415                420
10
     ACC GTC ATC CTC AAC CAG CTC ACC GAT CAG GAC GCC GGC TTC TAC TGG    1468
     Thr Val Ile Leu Asn Gln Leu Thr Asp Gln Asp Ala Gly Phe Tyr Trp
                 425                430                435

15   TGC GTG ACC GAC GGC GAC ACG CGC TGG ATC TCC ACA GTG GAG CTC AAG    1516
     Cys Val Thr Asp Gly Asp Thr Arg Trp Ile Ser Thr Val Glu Leu Lys
     440                445                450                455

     GTT GTC CAA GGA GAA CCA AGC CTC AAG GTA CCC AAG AAC GTC ACG GCT    1564
20   Val Val Gln Gly Glu Pro Ser Leu Lys Val Pro Lys Asn Val Thr Ala
                     460                465                470

     TGG CTG GGA GAG CCC TTA AAG CTC TCC TGC CAC TTC CCC TGC AAA TTC    1612
     Trp Leu Gly Glu Pro Leu Lys Leu Ser Cys His Phe Pro Cys Lys Phe
25                   475                480                485

     TAC TCC TTT GAG AAG TAC TGG TGT AAG TGG AGC AAC AGA GGC TGC AGC    1660
     Tyr Ser Phe Glu Lys Tyr Trp Cys Lys Trp Ser Asn Arg Gly Cys Ser
                 490                495                500
30
     GCC CTG CCC ACC CAG AAC GAC GGC CCC AGC CAG GCC TTT GTG AGC TGC    1708
     Ala Leu Pro Thr Gln Asn Asp Gly Pro Ser Gln Ala Phe Val Ser Cys
                 505                510                515

35   GAC CAG AAC AGC CAG GTC GTC TCC CTG AAC CTG GAC ACA GTC ACC AAG    1756
     Asp Gln Asn Ser Gln Val Val Ser Leu Asn Leu Asp Thr Val Thr Lys
     520                525                530                535

     GAG GAT GAA GGC TGG TAC TGG TGT GGA GTG AAG GAA GGC CCC CGA TAC    1804
40   Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Pro Arg Tyr
                     540                545                550

     GGG GAG ACG GCG GCT GTC TAC GTG GCA GTG GAG AGC AGG GTG AAG GGG    1852
     Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu Ser Arg Val Lys Gly
45                   555                560                565

     TCC CAA GGC GCC AAG CAA GTG AAA GCT GCC CCT GCG GGG GCG GCA ATA    1900
     Ser Gln Gly Ala Lys Gln Val Lys Ala Ala Pro Ala Gly Ala Ala Ile
                 570                575                580
50
     CAG TCG AGG GCC GGG GAG ATC CAG AAC AAA GCC CTT CTG GAC CCC AGC    1948
     Gln Ser Arg Ala Gly Glu Ile Gln Asn Lys Ala Leu Leu Asp Pro Ser
                 585                590                595

55   TTT TTC GCA AAG GAA AGT GTG AAG GAC GCT GCT GGT GGA CCC GGA GCA    1996
     Phe Phe Ala Lys Glu Ser Val Lys Asp Ala Ala Gly Gly Pro Gly Ala
     600                605                610                615

     CCT GCA GAT CCT GGC CGC CCT ACA GGA TAC AGC GGG AGC TCC AAA GCA    2044
60   Pro Ala Asp Pro Gly Arg Pro Thr Gly Tyr Ser Gly Ser Ser Lys Ala
                     620                625                630

     CTG GTC TCC ACC CTG GTG CCC CTG GCC CTG GTC CTG GTC GCA GGG GTC    2092
     Leu Val Ser Thr Leu Val Pro Leu Ala Leu Val Leu Val Ala Gly Val
65                   635                640                645
```

```
     GTG GCG ATC GGG GTG GTC CGA GCC CGG CAC AGG AAG AAC GTC GAC CGG    2140
     Val Ala Ile Gly Val Val Arg Ala Arg His Arg Lys Asn Val Asp Arg
             650             655             660

 5   ATT TCA ATC AGG AGC TAC CGG ACA GAT ATC AGC ATG TCA GAC TTT GAG    2188
     Ile Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu
             665             670             675

     AAC TCC AGG GAT TTT GAA GGA CGT GAC AAC ATG GGA GCC TCT CCA GAG    2236
10   Asn Ser Arg Asp Phe Glu Gly Arg Asp Asn Met Gly Ala Ser Pro Glu
     680             685             690             695

     GCC CAA GAG ACG TCT CTC GGA GGG AAG GAC GAG TTT GCC ACC ACT ACC    2284
     Ala Gln Glu Thr Ser Leu Gly Gly Lys Asp Glu Phe Ala Thr Thr Thr
15                   700             705             710

     GAG GAC ACC GTG GAG AGC AAA GAA CCC AAG AAG GCA AAG AGG TCG TCC    2332
     Glu Asp Thr Val Glu Ser Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser
                     715             720             725
20
     AAG GAG GAA GCC GAC GAG GCC TTC ACC ACC TTC CTC CTC CAG GCC AAA    2380
     Lys Glu Glu Ala Asp Glu Ala Phe Thr Thr Phe Leu Leu Gln Ala Lys
             730             735             740

25   AAC CTG GCC TCC GCC GCA ACC CAG AAC GGC CCG ACA GAA GCC TAG ACGGAG 2431
     Asn Leu Ala Ser Ala Ala Thr Gln Asn Gly Pro Thr Glu Ala
             745             750             755

     CCCTGGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAATCACGC TGATCCTCAG    2491
30
     GGCCCTCAGC TCGGGGGGCT CCACTGCCTG CACTCACACC CCGCCTAGGC TTCTCCTGTC    2551

     TGTCCTCAGA GGGTGTGCTG GTTCCTTCTT GGTGGCATCC AAGCCTGGCT TACTTGTTCC    2611

35   TATTGGGGGT GAGGTGGTAC GAGGAGTTCC CACCTGCAGC TTATTCGAAC GAGAGAACTA    2671

     AAGGTGTGGA GGAGAATTAA GATCGCAGAG GGGCCTCTCA GAAAGAAAAG GAGTGGGTGG    2731

     GGAGACAACC GCAGAAAGGG GGCCATTCAG CGCTTCCCTG TCCCCTTATT TGGGGATGTC    2791
40
     AGTGGAATCC TCCCTTCCAC CCCATCTCTG CACCTCTCCA TCCCCACTCC ATTCCATCTT    2851

     CTCTTCTTCT TTCCCTCATT AAAAATGTGC ATTTGGTTAC TCACTAGATT CCAGGGACTC    2911

45   TGCTAGACAC TGGGATAGGT AGGCCGCAAT CCCAGGCGGC AGCCTTCCGC AAACATCAAG    2971

     GAGCCCCTGG AGCCCACAGC ATCTCTTCAC GTGTACACTC ACTGACCTCT GCCTCTGCTG    3031

     GGAGAAATCA TAAAGGGTCT GCAGCCCTGA GGCCTTAGGG ATTATGTAAC ACAGGCATAC    3091
50
     ACACAAGGCA CCATCAACAC ATTCTTACCA TTTCACAGGT GAGAAAGCCG AGGTCCTGAG    3151

     AGGTGGAGAG GTTTGCTCAG AGTCAGCAAG TGAGATGTAC GAGTCTCAAG CTAAAGATTT    3211

55   GACACCTGCT GTCCCTACAG GAGGGCCTCC TCTCTCCAGA TGAGACAGCA TTCCATAGGA    3271

     AGGAGAAGAA AAATGTAAAT AAGACTGGTC TTTCACAGGC CCCACATCAG GGAAGATACC    3331

     CCTTTCCCTG TCTGTCACTC ACAGAGACCT AATAGGATAA GAGAATGGTC AACACTCAAA    3391
60
     CCCCCGAATG TGAAGAGTTC TAAGTGGAAA GGGAGGAAAA AGGGGGGATT TGATGGTGCC    3451

     AGGGAGGGGC TGATCTCCAA AGAACTAAGG TTTAAGTTTT TTTGTTTTTT TTTTCCTTC     3511

65   TTCTAAGCTC TGCACTTCAA CTAGCATCTA TGAGCTGGCA CTTGCTAACA AATCAAAAAT    3571
```

GTGAATTAAT TAATAATTAA AGACCATGAT TTCCTCCAAA AAAAAAAAAA AAAAAAAAA   3630

5   (2)   INFORMATION FOR SEQ ID NO: 6:

      (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 757 amino acids
10   (B)   TYPE: amino acid
        (C)   STRANDNESS: single
        (D)   TOPOLOGY: linear
          DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Ser Arg Leu Phe Leu Ala Cys Leu Leu Ala Ile Phe Pro Val Val
 1           5              10             15

Ser Met Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Ser Ser Val Glu
         20             25             30

Gly Arg Ser Val Ser Ile Lys Cys Tyr Tyr Pro Pro Thr Ser Val Asn
         35             40             45

Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Gln Gly Arg Cys
     50             55             60

Thr Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Asp Asp Tyr Val Gly
65             70             75             80

Arg Ala Asn Leu Thr Asn Phe Pro Glu Ser Gly Thr Phe Val Val Asp
             85             90             95

Ile Ser His Leu Thr His Lys Asp Ser Gly Arg Tyr Lys Cys Gly Leu
         100            105            110

Gly Ile Ser Ser Arg Gly Leu Asn Phe Asp Val Ser Leu Glu Val Ser
         115            120            125

Gln Asp Pro Ala Gln Ala Ser His Ala His Val Tyr Thr Ile Asp Leu
     130            135            140

Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Thr Arg Ala Asn Ser Glu
145            150            155            160

Lys Arg Lys Ser Leu Cys Lys Lys Thr Ile Gln Asp Cys Phe Gln Val
             165            170            175

Val Asp Ser Thr Gly Tyr Val Ser Asn Ser Tyr Lys Asp Arg Ala His
         180            185            190

Ile Ser Ile Leu Gly Thr Asn Thr Leu Val Phe Ser Val Val Ile Asn
         195            200            205

Arg Val Lys Leu Ser Asp Ala Gly Met Tyr Val Cys Gln Ala Gly Asp
     210            215            220

Asp Ala Lys Ala Asp Lys Ile Asn Ile Asp Leu Gln Val Leu Glu Pro
225            230            235            240

Glu Pro Glu Leu Val Tyr Gly Asp Leu Arg Ser Ser Val Thr Phe Asp
             245            250            255

Cys Ser Leu Gly Pro Glu Val Ala Asn Val Pro Lys Phe Leu Cys Gln
65             260            265            270
```

```
Lys Lys Asn Gly Gly Ala Cys Asn Val Val Ile Asn Thr Leu Gly Lys
        275             280             285

Lys Ala Gln Asp Phe Gln Gly Arg Ile Val Ser Val Pro Lys Asp Asn
5       290             295             300

Gly Val Phe Ser Val His Ile Thr Ser Leu Arg Lys Glu Asp Ala Gly
305             310             315             320

10  Arg Tyr Val Cys Gly Ala Gln Pro Glu Gly Glu Pro Gln Asp Gly Trp
                325             330             335

Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Thr Ala Ile Pro
        340             345             350
15

Ala Ser Pro Ser Val Val Lys Gly Val Arg Gly Gly Ser Val Thr Val
        355             360             365

Ser Cys Pro Tyr Asn Pro Lys Asp Ala Asn Ser Ala Lys Tyr Trp Cys
20      370             375             380

His Trp Glu Glu Ala Gln Asn Gly Arg Cys Pro Arg Leu Val Glu Ser
385             390             395             400

25  Arg Gly Leu Met Lys Glu Gln Tyr Glu Gly Arg Leu Val Leu Leu Thr
                405             410             415

Glu Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Asp
            420             425             430
30

Gln Asp Ala Gly Phe Tyr Trp Cys Val Thr Asp Gly Asp Thr Arg Trp
        435             440             445

Ile Ser Thr Val Glu Leu Lys Val Val Gln Gly Glu Pro Ser Leu Lys
35      450             455             460

Val Pro Lys Asn Val Thr Ala Trp Leu Gly Glu Pro Leu Lys Leu Ser
465             470             475             480

40  Cys His Phe Pro Cys Lys Phe Tyr Ser Phe Glu Lys Tyr Trp Cys Lys
                485             490             495

Trp Ser Asn Arg Gly Cys Ser Ala Leu Pro Thr Gln Asn Asp Gly Pro
            500             505             510
45

Ser Gln Ala Phe Val Ser Cys Asp Gln Asn Ser Gln Val Val Ser Leu
        515             520             525

Asn Leu Asp Thr Val Thr Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly
50      530             535             540

Val Lys Glu Gly Pro Arg Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala
545             550             555             560

55  Val Glu Ser Arg Val Lys Gly Ser Gln Gly Ala Lys Gln Val Lys Ala
                565             570             575

Ala Pro Ala Gly Ala Ala Ile Gln Ser Arg Ala Gly Glu Ile Gln Asn
        580             585             590
60

Lys Ala Leu Leu Asp Pro Ser Phe Phe Ala Lys Glu Ser Val Lys Asp
        595             600             605

Ala Ala Gly Gly Pro Gly Ala Pro Ala Asp Pro Gly Arg Pro Thr Gly
65      610             615             620
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     Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
     625             630             635             640
 5   Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
                 645             650             655
     His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
                 660             665             670
10   Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
                 675             680             685
     Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
                 690             695             700
15
     Asp Glu Phe Ala Thr Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
     705             710             715             720
20   Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
                 725             730             735
     Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
                 740             745             750
25   Gly Pro Thr Glu Ala
                 755
30
```

(2)   INFORMATION FOR SEQ ID NO: 7:

35
      (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 3095 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear
40   DESCRIPTION: Mouse Polyimmunoglobulin Receptor

      (ix)   FEATURE:

        (A)   NAME/KEY: Coding Sequence
45   (B)   LOCATION: 85....2400

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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50   TCACCTGGAG AGAAGGAAGT AGCTAAAACA TTCTCATACA AGAAGCCAAC CTGAGCGGCA      60

     CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG         111
                              Met Arg Leu Tyr Leu Phe Thr Leu Leu
                               1                   5
55   GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC       159
     Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro
     10              15              20              25
     CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC       207
60   Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
                 30              35              40
     TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA       255
     Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg
65               45              50              55
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      CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC      303
      Gln Gly Ala Ser Gly Met Cys Thr Thr Leu Ile Ser Ser Asn Gly Tyr
              60              65              70

  5   CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG      351
      Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu
              75              80              85

      AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT      399
 10   Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr
      90              95              100             105

      GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC      447
      Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe
 15           110             115             120

      GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC      495
      Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr
              125             130             135
 20
      CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT      543
      His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro
              140             145             150

 25   TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA      591
      Phe Lys Arg Glu Asn Val Pro Ser Lys Lys Ser Leu Cys Lys Lys Thr
              155             160             165

      AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC      639
 30   Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro
      170             175             180             185

      AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGG ACC GAC CTA ACT      687
      Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr
 35           190             195             200

      GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGG CTG      735
      Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu
              205             210             215
 40
      TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT      783
      Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val
              220             225             230

 45   GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG      831
      Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu
              235             240             245

      AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC      879
 50   Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn
      250             255             260             265

      GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC      927
      Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile
 55           270             275             280

      ATT AAC ACC CTG GGG AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG      975
      Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu
              285             290             295
 60
      ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC      1023
      Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly
              300             305             310

 65   CTG AGG AAG GAG GAT GCA GGG CAC TAC CAG TGT GGA GCC CAC AGT TCT      1071
      Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser
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                315                  320                   325

     GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC    1119
     Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val
 5   330                 335                 340                 345

     AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC    1167
     Asn Glu Glu Ser Thr Ile Pro Asn Arg Arg Ser Val Val Lys Gly Val
                     350                 355                 360
10

     ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC    1215
     Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser
                 365                 370                 375

15   AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT    1263
     Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His
                 380                 385                 390

     TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA    1311
20   Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu
                 395                 400                 405

     GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC    1359
     Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val
25   410                 415                 420                 425

     ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT    1407
     Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu
                     430                 435                 440
30

     ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC    1455
     Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala
                 445                 450                 455

35   GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA    1503
     Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr
                 460                 465                 470

     GCA GTA CTA GGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA    1551
40   Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys
                 475                 480                 485

     TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC    1599
     Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Lys Gly Cys
45   490                 495                 500                 505

     CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC    1647
     His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser
                     510                 515                 520
50

     TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT    1695
     Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser
                 525                 530                 535

55   AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC    1743
     Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr
                 540                 545                 550

     TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA    1791
60   Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg
                 555                 560                 565

     GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC    1839
     Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val
65   570                 575                 580                 585
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    GCT CTG GAA GAA GAG GTA GTG GAC TCC TCC ATC AGT GAA AAA GAG AAC      1887
    Ala Leu Glu Glu Glu Val Val Asp Ser Ser Ile Ser Glu Lys Glu Asn
                    590                 595                 600

 5  AAA GCC ATT CCA AAT CCC GGG CCT TTT GCC AAC GAA AGA GAG ATA CAG      1935
    Lys Ala Ile Pro Asn Pro Gly Pro Phe Ala Asn Glu Arg Glu Ile Gln
                605                 610                 615

    AAT GTG AGA GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG GAT GCT GGC      1983
10  Asn Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly
                620                 625                 630

    AGT GCT GAT GGA CAA AGC AGG AGC TCC AGC TCC AAA GTG CTG TTC TCC      2031
    Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Ser Lys Val Leu Phe Ser
15          635                 640                 645

    ACC CTG GTG CCC CTG GGT CTG GTG CTG GCA GTG GGT GCT ATA GCT GTG      2079
    Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Ile Ala Val
    650                 655                 660                 665

20
    TGG GTG GCC AGA GTC CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC      2127
    Trp Val Ala Arg Val Arg His Arg Lys Asn Val Asp Arg Met Ser Ile
                    670                 675                 680

25  AGC AGC TAC AGG ACA GAC ATT AGC ATG GCA GAC TTC AAG AAC TCC AGA      2175
    Ser Ser Tyr Arg Thr Asp Ile Ser Met Ala Asp Phe Lys Asn Ser Arg
                    685                 690                 695

    GAT TTG GGA GGC AAT GAC AAC ATG GGG GCC TCT CCA GAC ACA CAG CAA      2223
30  Asp Leu Gly Gly Asn Asp Asn Met Gly Ala Ser Pro Asp Thr Gln Gln
                700                 705                 710

    ACA GTC ATC GAA GGA AAA GAT GAA ATC GTG ACT ACC ACG GAG TGC ACC      2271
    Thr Val Ile Glu Gly Lys Asp Glu Ile Val Thr Thr Thr Glu Cys Thr
35          715                 720                 725

    GCT GAG CCA GAA GAA TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA      2319
    Ala Glu Pro Glu Glu Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu
    730                 735                 740                 745

40
    GCT GAC ATG GCC TAC TCG GCA TTC CTG CTT CAG TCC AGC ACC ATA GCT      2367
    Ala Asp Met Ala Tyr Ser Ala Phe Leu Leu Gln Ser Ser Thr Ile Ala
                    750                 755                 760

45  GCA CAG GTC CAC GAT GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCCACCC   2420
    Ala Gln Val His Asp Gly Pro Gln Glu Ala
                765                 770

    TTGCCTGTGA CAATCAACTT GAGAATCACA CTGATCCGCT CGCAGCCCAC ACTCACCCAT   2480
50
    CACCTCCGCT CTTCCCTCCT GTCCTCAGAG GTGTGCTGGT TCCTTCCTCG GCCATGGAAG   2540

    CCTGGCCTAG TTACGCCTGT TTAGGAGAGA GTGTGAGGCG TTCTTTTCTC TATGAAGAGA   2600

55  GTGAGGTGGA AATGAGGAGG AGGTGAACCT GAGAGACATC TCTGGAGGAA GAGGGTTGAG   2660

    AATAGGGGCT CGTTTCAGGA GAAAAGGCCA TTTGAATCTT CTTTATAACC ATATGATAGG   2720

    ATGTCAGCGT AACTCTTCTC TCCTCCATCT CTCCTTTCCT ATCCTCTTGA TTCAAACAAC   2780
60
    ACATCTGAGA ACTCACTAGG CTTCAGTGCC TACTAAATGC TGAGAGCCAG GCCACAATCT   2840

    TTCTATAAAT ATTACTGGAA GAGATGCCAT CTCCTCCCAG ATTCTGTCTT TTCATTAAGA   2900

65  TAAGACATCA TTACCAGGCA TACCTCCTGC CTCTGTGCCT CATAGGCATA CACAAGCCAT   2960
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AAGGGCATCA TGATTTTCAG ATGAGAAGAG ATGTTTCTCA AGAGTGCCTA GTGAGATAGA   3020

CTAGCGTCAA ACCAGATGTG GCAACTCCTG GCTCTTGGCC TACGATCTGT CTTCAAGAAA   3080

5 AAAAAAAAAA AAAAA   3095

(2) INFORMATION FOR SEQ ID NO: 8:

10
        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 771 amino acids
            (B) TYPE: amino acid
15   (C) STRANDNESS: single
            (D) TOPOLOGY: linear
                DESCRIPTION: Mouse Polyimmunoglobulin Receptor

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
20
    Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val
    1   5   10   15

    Ser Thr Lys Ser Pro Ile Phe Gly Pro Gln Glu Val Ser Ser Ile Glu
25   20   25   30

    Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
                35   40   45

30 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys
            50   55   60

    Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
    65   70   75   80
35
    Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn
                85   90   95

    Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu
40   100   105   110

    Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
                115   120   125

45 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile
            130   135   140

    Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro
    145   150   155   160
50
    Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val
                165   170   175

    Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys
55   180   185   190

    Leu Phe Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser
                195   200   205

60 His Leu Thr His Asn Asp Ala Gly Leu Tyr Ile Cys Gln Ala Gly Glu
            210   215   220

    Gly Pro Ser Ala Asp Lys Lys Asn Val Asp Leu Gln Val Leu Ala Pro
    225   230   235   240
65
    Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu

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                    245                 250                 255

        Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg
  5                 260                 265                 270

        Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg
                    275                 280                 285

        Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn
 10         290                 295                 300

        Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly
        305                 310                 315                 320

 15     His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp
                        325                 330                 335

        Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro
 20                 340                 345                 350

        Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile
                    355                 360                 365

 25     Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys
            370                 375                 380

        Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr
        385                 390                 395                 400

 30     Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp
                        405                 410                 415

        Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr
 35                 420                 425                 430

        Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp
                435                 440                 445

 40     Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn
            450                 455                 460

        Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe
        465                 470                 475                 480

 45     Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr
                    485                 490                 495

        Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp
 50                 500                 505                 510

        Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu
                515                 520                 525

 55     Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr
            530                 535                 540

        Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile
        545                 550                 555                 560

 60     Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro
                    565                 570                 575

        Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Glu Val Val
                    580                 585                 590
 65
        Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly
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                595                   600                   605
      Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln
5         610                 615                 620

      Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg
      625                 630                 635                 640

10    Ser Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu
                      645                 650                 655

      Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His
                  660                 665                 670
15    Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile
              675                 680                 685

      Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn
          690                 695                 700
20    Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp
      705                 710                 715                 720

      Glu Ile Val Thr Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys
25                    725                 730                 735

      Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala
                  740                 745                 750
30    Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro
              755                 760                 765

      Gln Glu Ala
          770
35
```

(2)   INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 3269 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear
        DESCRIPTION: Rat Polyimmunoglobulin Receptor

    (ix)   FEATURE:

        (A)   NAME/KEY: Coding Sequence
        (B)   LOCATION: 74....2383

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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GGCAACGAAG GTACCATGGA TCTTATACAA GAAGTGAACC AACATGCCGC AACCTCCTTG          60

GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC            109
              Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val
              1               5                   10

TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG          157
Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val
        15                  20                  25

AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC          205
Ser Ser Ile Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp
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                30                    35                   40

        ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA CAA GGA GCC         253
        Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala
  5     45              50              55              60

        AAC GGC TAC TGC GCA ACC CTC ATC TCT TCA AAT GGC TAC CTC TCG AAG         301
        Asn Gly Tyr Cys Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys
                        65              70              75
  10

        GAG TAT TCA GGC AGA GCC AGC CTC ATC AAC TTC CCA GAG AAT AGC ACA         349
        Glu Tyr Ser Gly Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr
                        80              85              90

  15    TTT GTG ATT AAC ATT GCA CAT CTC ACC CAG GAG GAC ACT GGG AGC TAC         397
        Phe Val Ile Asn Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr
                        95              100             105

        AAG TGT GGT CTG GGT ACC ACT AAC CGA GGC CTG TTT TTC GAT GTC AGC         445
  20    Lys Cys Gly Leu Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser
            110             115             120

        CTG GAG GTC AGC CAG GTT CCT GAG TTC CCA AAT GAC ACC CAT GTC TAC         493
        Leu Glu Val Ser Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr
  25    125             130             135             140

        ACA AAG GAC ATA GGC AGA ACT GTG ACC ATC GAA TGC CGT TTC AAA GAG         541
        Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu
                        145             150             155
  30

        GGG AAT GCT CAT AGC AAG AAA TCC CTG TGT AAG AAG AGA GGA GAG GCC         589
        Gly Asn Ala His Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala
                        160             165             170

  35    TGC GAA GTT GTC ATC GAC TCT ACT GAG TAC GTG GAC CCC AGC TAT AAG         637
        Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys
                        175             180             185

        GAC AGA GCA ATC CTT TTT ATG AAA GGG ACC AGC CGC GAT ATA TTC TAT         685
  40    Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr
                        190             195             200

        GTC AAC ATT AGC CAC CTA ATA CCC AGT GAT GCT GGA CTG TAT GTT TGC         733
        Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys
  45    205             210             215             220

        CAA GCT GGA GAA GGC CCC AGT GCT GAT AAA AAT AAT GCT GAC CTC CAG         781
        Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln
                        225             230             235
  50

        GTG CTA GAG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG AGG TCC TCA         829
        Val Leu Glu Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser
                        240             245             250

  55    GTG ACT TTT GAA TGT GAC CTG GGC CGT GAA GTG GCA AAT GAT GCC AAA         877
        Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys
                        255             260             265

        TAT CTG TGT CGG AAG AAC AAG GAA ACC TGT GAT GTC ATC ATC AAC ACC         925
  60    Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr
            270             275             280

        CTG GGG AAG AGA GAT CCA GCC TTT GAA GGC AGG ATC CTG CTA ACC CCC         973
        Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro
  65    285             290             295             300
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     AGG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC CTG AGG AAG      1021
     Arg Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys
                     305                 310                 315

  5  GAG GAT GCA GGG CAC TAC CAG TGT GGA GCG CAC AGT TCT GGT TTG CCT      1069
     Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro
                     320                 325                 330

     CAA GAA GGC TGG CCC GTC CAG GCT TGG CAA CTC TTT GTC AAT GAA GAG      1117
 10  Gln Glu Gly Trp Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu
                     335                 340                 345

     TCC ACG ATT CCC AAT AGT CGC TCT GTT GTG AAG GGT GTC ACA GGA GGC      1165
     Ser Thr Ile Pro Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly
 15      350                 355                 360

     TCT GTG GCC ATC GTC TGT CCC TAT AAC CCC AAG GAA AGC AGC AGC CTC      1213
     Ser Val Ala Ile Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu
     365                 370                 375                 380
 20
     AAG TAC TGG TGT CAC TGG GAA GCC GAC GAG AAT GGA CGC TGC CCG GTG      1261
     Lys Tyr Trp Cys His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val
                     385                 390                 395

 25  CTC GTG GGG ACC CAG GCC CTG GTG CAA GAA GGA TAT GAA GGC CGA CTG      1309
     Leu Val Gly Thr Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu
                     400                 405                 410

     GCA CTG TTC GAT CAG CCG GGC AGT GGC GCC TAC ACT GTC ATC CTC AAC      1357
 30  Ala Leu Phe Asp Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn
                     415                 420                 425

     CAG CTC ACC ACC CAG GAT TCT GGC TTC TAC TGG TGT CTT ACC GAT GGT      1405
     Gln Leu Thr Thr Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly
 35      430                 435                 440

     GAC TCT CGC TGG AGA ACC ACG ATA GAA CTG CAG GTT GCT GAA GCT ACA      1453
     Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr
     445                 450                 455                 460
 40
     AAG AAG CCA GAC CTT GAG GTG ACA CCA CAG AAC GCG ACC GCG GTG ATA      1501
     Lys Lys Pro Asp Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile
                     465                 470                 475

 45  GGA GAG ACC TTC ACA ATC TCC TGC CAC TAT CCG TGC AAA TTC TAC TCC      1549
     Gly Glu Thr Phe Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser
                     480                 485                 490

     CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC GAC GGC TGC CAC ATC CTG      1597
 50  Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu
                     495                 500                 505

     CCG AGC CAT GAT GAA GGT GCC CGC CAG TCC TCT GTG AGC TGT GAC CAG      1645
     Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln
 55      510                 515                 520

     AGC AGC CAG ATC GTC TCC ATG ACC CTG AAC CCG GTC AAA AAG GAA GAT      1693
     Ser Ser Gln Ile Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp
     525                 530                 535                 540
 60
     GAA GGC TGG TAC TGG TGT GGG GTA AAA GAA GGT CAG GTC TAT GGA GAA      1741
     Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu
                     545                 550                 555

 65  ACT ACA GCC ATC TAT GTA GCA GTT GAA GAG AGG ACC AGA GGG TCA CCC      1789
     Thr Thr Ala Ile Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro
```

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                    560                      565                      570

      CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG    1837
 5    His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu
              575                 580                 585

      GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT    1885
      Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn
              590                 595                 600
10
      CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA    1933
      Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly
      605                 610                 615                 620

15    GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT    1981
      Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly
                          625                 630                 635

      GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG    2029
20    Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu
                      640                 645                 650

      GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC    2077
      Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val
25                655                 660                 665

      CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA    2125
      Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr
              670                 675                 680
30
      GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GGC AAT    2173
      Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn
      685                 690                 695                 700

35    GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA    2221
      Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly
                          705                 710                 715

      AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA    2269
40    Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu
                      720                 725                 730

      TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC    2317
      Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr
45            735                 740                 745

      TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT    2365
      Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp
              750                 755                 760
50
      GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT  2422
      Gly Pro Gln Glu Ala
      765

55    TGAGAATCAC ATTGATCCAC TCGCAGCCCA CCCTCGCCCA TCACCCAGGC TCTTCCCTCC   2482

      TGTTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG   2542

      TTTAGGAGAG AGCGTGAGGA GTTCTTTTTG CTGTTAAAGA GTAAGGTGGA AATGAGTTGA   2602
60
      GCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTC AGGAGGAAGA   2662

      GCCATTTGAA GCCTCTTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT   2722

65    CTCTCCTTTC TTCTCTTCTT GATTCAGACA ACAGATCCGA AAACTCACTA GGCTTCCGGT   2782
```

```
GTCTACTAAA TGCTGAGAGT CAGGCCACAG CCTTTCTATA AACATCACTG GAAGAGACAC  2842

CACCTCGTCC CAGATTCTGT CTTTTCCCTA AGCTATCAAT CATTACCGGG GATTCCCTTT  2902

GCCTCTGCAC CTCATAGGCA ACAAAAGAAA CATAAGTCCT GCAGTCTAAG GCATACCCAA  2962

GCCATAAGGG CACCACGAGA CTCAGATGAG AAGAGATTTT TCTCCAGAGT ACTCAGTGAG  3022

ATAGACTAGT GTCAAGCCAG ATGGGGCAAC TCCTGGCTCT TGGCCTGGGA CTTGTCTTCA  3082

AGATCTCTGC TCTTATTAGA GAAAGAACTT TAGCATGAGG AAAAGTAAGA GAAAACAAGT  3142

TACATGGGCA TGGTGGTGTG CTCCTGCAAT CCCAATATTA AGAGGTTAAA AAATAGGACC  3202

AGAAGTTTAA AGTAATCCTT GGCTACCTAG TGAGTGTAAG GCCAGCCTGG AATCAATAAG  3262

AGTTGGT                                                             3269
```

(2)   INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 770 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDNESS: single
        (D)   TOPOLOGY: linear
        DESCRIPTION: Rat Polyimmunoglobulin Receptor

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val
 1               5                  10                  15

Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu
            20              25                  30

Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
        35                  40                  45

Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
    50                  55                  60

Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
65                  70                  75                  80

Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn
                85                  90                  95

Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu
            100                 105                 110

Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser
        115                 120                 125

Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile
    130                 135                 140

Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His
145                 150                 155                 160

Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val
                165                 170                 175

Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile
```

```
                   180                  185                  190

      Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser
              195             200             205
  5

      His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu
              210             215             220

      Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro
 10   225             230             235             240

      Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu
                  245             250             255

 15   Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg
                  260             265             270

      Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg
              275             280             285
 20

      Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn
          290             295             300

      Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly
 25   305             310             315             320

      His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp
                  325             330             335

 30
      Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro
              340             345             350

      Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile
 35           355             360             365

      Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys
          370             375             380

 40   His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val Leu Val Gly Thr
      385             390             395             400

      Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu Ala Leu Phe Asp
              405             410             415
 45

      Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr
              420             425             430

      Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly Asp Ser Arg Trp
 50           435             440             445

      Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Lys Lys Pro Asp
          450             455             460

 55   Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile Gly Glu Thr Phe
      465             470             475             480

      Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr
                  485             490             495

 60
      Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu Pro Ser His Asp
              500             505             510

      Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Ile
 65           515             520             525
```

```
     Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
         530             535             540

  5  Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
     545             550             555             560

     Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
                     565             570             575

 10  Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Glu Ala Met
                 580             585             590

     Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
         595             600             605

 15  Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
         610             615             620

     Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 20  625             630             635             640

     Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
                 645             650             655

 25  Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
                 660             665             670

     Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
                 675             680             685

 30  Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
         690             695             700

     Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 35  705             710             715             720

     Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
                 725             730             735

 40  Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
                 740             745             750

     Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
         755             760             765

 45  Ala
```

50 (2) INFORMATION FOR SEQ ID NO: 11:

          (i) SEQUENCE CHARACTERISTICS:

               (A)   LENGTH: 322 base pairs
55   (B)   TYPE: nucleic acid
               (C)   STRANDEDNESS: single
               (D)   TOPOLOGY: linear
                      DESCRIPTION: Guy's 13 Kappa

60   (ix) FEATURE:

               (A)   NAME/KEY: Coding Sequence
               (B)   LOCATION: 8....320

65   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
     CTCGAGC GAC ATT GTG ATG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT       49
             Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
              1               5                   10
```

```
  5  CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT GCC AGC TCA AGT GTA AGT       97
     Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
     15                  20              25                  30
```

```
     TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC ACT TCT CCC AAA CTC TGG      145
 10  Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp
                     35                  40                  45
```

```
     CTT TAT AGC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT      193
     Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 15                  50                  55                  60
```

```
     GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC CGA ATG GAG      241
     Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu
                     65                  70                  75
 20
```

```
     GCT GAA GAT GCT GCC ACT TAT TAC TGC CAT CAA AGG ACT AGT TAC CCG      289
     Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro
                 80                  85                  90
```

```
 25  TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA A TA                         322
     Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
     95                  100                 105
```

30 (2)   INFORMATION FOR SEQ ID NO: 12:

               (i)   SEQUENCE CHARACTERISTICS:

                       (A)   LENGTH: 105 amino acids
35   (B)   TYPE: amino acid
                       (C)   STRANDNESS: single
                       (D)   TOPOLOGY: linear
                        DESCRIPTION: Guy's 13 Kappa

40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
     Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
      1               5                   10                  15
```

```
45   Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
                     20              25                  30
```

```
     His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr
                 35                  40                  45
50
```

```
     Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
                 50                  55                  60
```

```
     Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
55   65                  70                  75                  80
```

```
     Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr
                     85                  90                  95
```

```
60   Phe Gly Gly Gly Thr Lys Leu Glu Ile
                     100                 105
```

65
     (2)   INFORMATION FOR SEQ ID NO: 13:

(i)   SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 402 base pairs
    (B)   TYPE: nucleic acid
    (C)   STRANDEDNESS: single
    (D)   TOPOLOGY: linear
       DESCRIPTION: Guy's 13 Gamma 1

(ix)   FEATURE:

    (A)   NAME/KEY: Coding Sequence
    (B)   LOCATION: 7...402

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
CTCGAG ATG GAA TGG ACC TGG GTT TTT CTC TTC CTC CTG TCA GGA ACT      48
       Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr
        1           5                  10

GCA GGC GTC CAC TCT GGG GTC CAG CTT CAG CAG TCA GGA CCT GAC CTG      96
Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
 15              20                  25                  30

GTG AAA CCT GGG GCC TCA GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC     144
Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
                35                  40                  45

ACA TTC ACT GAC TAC AAC ATA CAC TGG GTG AAG CAG AGC CGT GGA AAG     192
Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys
            50                  55                  60

AGC CTT GAG TGG ATT GGA TAT ATT TAT CCT TAC AAT GGT AAT ACT TAC     240
Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr
            65                  70                  75

TAC AAC CAG AAG TTC AAG AAC AAG GCC ACA TTG ACT GTA GAC AAT TCC     288
Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser
            80                  85                  90

TCC ACC TCA GCC TAC ATG GAG CTC CGC AGC CTG ACA TCT GAG GAC TCT     336
Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
 95                 100                 105                 110

GCA GTC TAT TAC TGT GCA ACC TAC TTT GAC TAC TGG GGC CAA GGC ACC     384
Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
                115                 120                 125

ACT CTC ACA GTC TCC TCA                                             402
Thr Leu Thr Val Ser Ser
            130
```

(2)   INFORMATION FOR SEQ ID NO: 14:

(i)   SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 132 amino acids
    (B)   TYPE: amino acid
    (C)   STRANDNESS: single
    (D)   TOPOLOGY: linear
       DESCRIPTION: Guy's 13 Gamma 1

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1           5               10                  15

Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
             20              25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
             35              40                  45

Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
     50              55                  60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65              70                  75                      80

Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
             85              90                  95

Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
            100             105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
        115             120                 125

Thr Val Ser Ser
    130
```

(2)   INFORMATION FOR SEQ ID NO: 15:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 31 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGATCTA TGGAATGGAC CTGGGTTTTT C   31

(2)   INFORMATION FOR SEQ ID NO: 16:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCAAGCTTG GTTTTGGAGA TGGTTTTCTC   30

(2)   INFORMATION FOR SEQ ID NO: 17:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 31 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATAAGCTTG GTCCTACTCC TCCTCCTCCT A   31

(2)   INFORMATION FOR SEQ ID NO: 18:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATCTCGAGT CAGTAGCAGA TGCCATCTCC   30

(2)   INFORMATION FOR SEQ ID NO: 19:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGAAAGCTTT GTACATATGC AAGGCTTACA   30